



SEQUENCE LISTING

<110> Odgren, Paul R.
Marks, Sandy C.
Choi, Yongwon

<120> TRANCE REGULATION OF CHONDROCYTE
DIFFERENTIATION

<130> 07917-120001

<140> 09/933,915

<141> 2001-08-20

<150> 60/226,197

<151> 2000-08-18

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2226

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (157)...(1107)

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agggaggaga	gctccgaagc	gagagggccg	agcgcc atg	cgc cgc gcc agc aga		174
			Met Arg Arg Ala Ser Arg			
			1	5		

gac tac acc aag tac ctg cgt ggc tgc gag gag atg ggc ggc ggc ccc	222
Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu Glu Met Gly Gly Gly Pro	
10 15 20	

gga gcc ccg cac gag ggc ccc ctg cac gcc ccg ccg ccg cct gcg ccg	270
Gly Ala Pro His Glu Gly Pro Leu His Ala Pro Pro Pro Pro Ala Pro	
25 30 35	

cac cag ccc ccc gcc gcc tcc cgc tcc atg ttc gtg gcc ctc ctg ggg	318
His Gln Pro Pro Ala Ala Ser Arg Ser Met Phe Val Ala Leu Leu Gly	
40 45 50	

ctg ggg ctg ggc cag gtt gtc tgc agc gtc gcc ctg ttc ttc tat ttc	366
Leu Gly Leu Gly Gln Val Val Cys Ser Val Ala Leu Phe Phe Tyr Phe	
55 60 65 70	

aga gcg cag atg gat cct aat aga ata tca gaa gat ggc act cac tgc	414
Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys	
75 80 85	



1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYF
71 RAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHI
141 RAEKAMVDGSWLDLAKRSKLEAQPF AHL TINATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQ
211 DGFYYLYANICFRHHETSGDLATEYLQIMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF
281 FKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID (SEQ ID NO:2)

FIG. 2

att tat aga att ttg aga ctc cat gaa aat gca gat ttt caa gac aca Ile Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr 90 95 100	462
act ctg gag agt caa gat aca aaa tta ata cct gat tca tgt agg aga Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg 105 110 115	510
att aaa cag gcc ttt caa gga gct gtg caa aag gaa tta caa cat atc Ile Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile 120 125 130	558
gtt gga tca cag cac atc aga gca gag aaa gcg atg gtg gat ggc tca Val Gly Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser 135 140 145 150	606
tgg tta gat ctg gcc aag agg agc aag ctt gaa gct cag cct ttt gct Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala 155 160 165	654
cat ctc act att aat gcc acc gac atc cca tct ggt tcc cat aaa gtg His Leu Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val 170 175 180	702
agt ctg tcc tct tgg tac cat gat cgg ggt tgg gcc aag atc tcc aac Ser Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn 185 190 195	750
atg act ttt agc aat gga aaa cta ata gtt aat cag gat ggc ttt tat Met Thr Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr 200 205 210	798
tac ctg tat gcc aac att tgc ttt cga cat cat gaa act tca gga gac Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp 215 220 225 230	846
cta gct aca gag tat ctt caa cta atg gtg tac gtc act aaa acc agc Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser 235 240 245	894
atc aaa atc cca agt tct cat acc ctg atg aaa gga gga agc acc aag Ile Lys Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys 250 255 260	942
tat tgg tca ggg aat tct gaa ttc cat ttt tat tcc ata aac gtt ggt Tyr Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly 265 270 275	990
gga ttt ttt aag tta cgg tct gga gag gaa atc agc atc gag gtc tcc Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser 280 285 290	1038
aac ccc tcc tta ctg gat ccg gat cag gat gca aca tac ttt ggg gct Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala 295 300 305 310	1086

ttt aaa gtt cga gat ata gat tgagccccag tttttggagt gttatgtatt 1137
 Phe Lys Val Arg Asp Ile Asp
 315

tcctggatgt ttggaaacat tttttaaaac aagccaagaa agatgtatat aggtgtgtga 1197
 gactactaag aggcattggc ccaacggtac acgactcagt atccatgctc ttgaccttgt 1257
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 attccctggg gaaaacttgc agctaaggag gggaaaaaaa tgttgtttcc taatatcaaa 1797
 tgcagtatat ttcttcgttc tttttaagtt aatagatttt ttcagacttg tcaagcctgt 1857
 gcaaaaaaat taaaatggat gccttgaata ataagcagga tgttggccac caggtgcctt 1917
 tcaaatattg aaactaattg actttagaaa gctgacattg ccaaaaagga tacataatgg 1977
 gccactgaaa tctgtcaaga gtagttatat aattgttgaa caggtgtttt tccacaagtg 2037
 ccgcaaattg tacctttttt tttttttcaa aatagaaaag ttattagtgg tttatcagca 2097
 aaaaagtcca attttaattt agtaaatgtt atcttatact gtacaataaa aacattgcct 2157
 ttgaatgtta attttttggt acaaaaataa atttatatga aaacctgaaa aaaaaaacia 2217
 aaaaaaaaaa 2226

<210> 2
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
 1 5 10 15
 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
 20 25 30
 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 35 40 45
 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 50 55 60
 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80
 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85 90 95
 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His

210	215	220
His Glu Thr Ser Gly Asp	Leu Ala Thr Glu Tyr	Leu Gln Leu Met Val
225	230	235
Tyr Val Thr Lys Thr Ser	Ile Lys Ile Pro Ser	Ser His Thr Leu Met
245	250	255
Lys Gly Gly Ser Thr Lys	Tyr Trp Ser Gly Asn	Ser Glu Phe His Phe
260	265	270
Tyr Ser Ile Asn Val Gly	Gly Phe Phe Lys Leu	Arg Ser Gly Glu Glu
275	280	285
Ile Ser Ile Glu Val Ser	Asn Pro Ser Leu Leu	Asp Pro Asp Gln Asp
290	295	300
Ala Thr Tyr Phe Gly Ala	Phe Lys Val Arg Asp	Ile Asp
305	310	315

<210> 3
 <211> 192
 <212> PRT
 <213> Homo Sapiens

<400> 3
Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg
1 5 10 15
Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg
20 25 30
Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr
35 40 45
Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His
50 55 60
Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys
65 70 75 80
Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys
85 90 95
Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln
100 105 110
Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His
115 120 125
Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu
130 135 140
Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser
145 150 155 160
Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro
165 170 175
Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
180 185 190

<210> 4
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 4
Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
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Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
20 25 30
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
35 40 45

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
 50 55 60
 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
 65 70 75 80
 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
 85 90 95
 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
 100 105 110
 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
 115 120 125
 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
 130 135 140
 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
 145 150 155 160
 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
 165 170 175
 Val Arg Asp Ile Asp
 180

<210> 5
 <211> 178
 <212> PRT
 <213> Homo sapiens

<400> 5
 Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala
 1 5 10 15
 Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
 20 25 30
 Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp
 35 40 45
 Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn
 50 55 60
 Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
 65 70 75 80
 Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr
 85 90 95
 Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser
 100 105 110
 Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn
 115 120 125
 Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu
 130 135 140
 Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu
 145 150 155 160
 Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp
 165 170 175
 Ile Asp

<210> 6
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 6
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu

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Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro	
			20					25					30			
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
		35					40					45				
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val	
	50					55					60					
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
65					70					75					80	
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val	
				85					90					95		
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met	
			100					105					110			
Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
		115					120					125				
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu	
	130					135					140					
Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
145					150					155					160	
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp				
				165					170							

<210> 7
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 7																
Ser	Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	
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Asp	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	
		20						25					30			
Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	
		35					40					45				
Leu	Ile	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	
	50					55					60					
Phe	Arg	His	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	
65					70					75					80	
Leu	Met	Val	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	
				85					90					95		
Thr	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	
			100					105				110				
Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	
		115					120					125				
Gly	Glu	Glu	Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	
	130					135					140					
Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp	
145					150					155					160	

<210> 8
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 8																
Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	
1				5					10					15		

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Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp
      20      25      30
Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu
      35      40      45
Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe
      50      55      60
Arg His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu
      65      70      75      80
Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr
      85      90      95
Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe
      100      105      110
His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly
      115      120      125
Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp
      130      135      140
Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
      145      150      155

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<210> 9
<211> 1945
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (95)...(826)

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<221> misc_feature
<222> (1)...(1945)
<223> n = A,T,C or G

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tcaacaacac ttagaagcca ccaaagaatt gcag atg gat cct aat aga ata tca      115
                               Met Asp Pro Asn Arg Ile Ser
                               1               5

gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa aat      163
Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
      10      15      20

gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta ata      211
Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
      25      30      35

cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg caa      259
Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
      40      45      50      55

aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag aaa      307
Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
      60      65      70

gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag ctt      355
Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
      75      80      85

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gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc cca Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro 90 95 100	403
tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg ggt Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly 105 110 115	451
tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata gtt Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val 120 125 130 135	499
aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga cat Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 140 145 150	547
cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg gtg His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val 155 160 165	595
tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg atg Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met 170 175 180	643
aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat ttt Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe 185 190 195	691
tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag gaa Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu 200 205 210 215	739
atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag gat Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp 220 225 230	787
gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tgagccccag Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp 235 240	836
tttttgaggt gttatgtatt tcttgatgt ttggaacat tttttaaac aagccaagaa agatgtatat aggtgtgtga gactactaag aggcattggc ccaacggtac acgactcagt atccatgctc ttgacctgt agagaacacg cgtattttaca gccagtggga gatgttagac tcatggtgtg ttacacaatg gtttttaaat tttgtaatga attcctagaa ttaaaccaga ttggagcaat tacgggttga ccttatgaga aactgcatgt gggctatggg aggggttgg ccctggtcat gtgccccctt gcagctgaag ttggagagggt gtcattctagc gcaattgaag gatcatctga aggggcaaat tcttttgaat tggttacatca tgctggaacc tgcaaaaaat actttttcta atgaggagag aaaatatatg tatttttata taatatctaa agttatattt cagatgtaat gttttctttg caaagtattg taaattatat ttgtgctata gtatttgatt caaaatattt aaaaatgtct tgctgttgac atatttaatg ttttaaatgt acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag gggaaaaaaa tggtgtttcc taatatcaaa tgcagtatat ttcttoggct tttttaagtt aatagatttt ttcagacttg tcaagcctgt gcaaaaaaat taaaatggat gccttgaata ataagcagga tggtggccac cagggtgcctt tcaaatttag aaactaattg acttttagaaa gctgacattg ccaaaaagga tacataatgg gccactgaaa tctgtcaaga gtagttatat aattgttgaa cagggtgtttt tccacaagtg ccgcaaattg tacctttttt tttttttcaa aatagaaaag	896 956 1016 1076 1136 1196 1256 1316 1376 1436 1496 1556 1616 1676 1736 1796

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ttattagtgg tttatcagca aaaaagtcca attttaattt agtaaagtgtt atcttatact 1856
gtacaataaaa aacattgcct ttgaatgtta attttttggt acaaaaataa atttatatga 1916
aaacctgaaa aaaaaaaciaa aaaaaaaaaa 1945

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<210> 10
<211> 244
<212> PRT
<213> Homo sapiens

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1          5          10          15
Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu
20        25        30
Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln
35        40        45
Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Ser
50        55        60
Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu Asp
65        70        75        80
Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu Thr
85        90        95
Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu Ser
100       105       110
Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Phe
115       120       125
Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr
130       135       140
Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala Thr
145       150       155       160
Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys Ile
165       170       175
Pro Ser Ser His Thr Leu Met Lys Gly Ser Thr Lys Tyr Trp Ser
180       185       190
Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe
195       200       205
Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro Ser
210       215       220
Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val
225       230       235       240
Arg Asp Ile Asp

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<210> 11
<211> 3136
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (39)...(1886)

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<400> 11
ccgctgaggc cgcggcgccc gccagcctgt cccgcgcc atg gcc ccg cgc gcc cgg 56
Met Ala Pro Arg Ala Arg
1          5

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cgg cgc cgc ccg ctg ttc gcg ctg ctg ctg ctc tgc gcg ctg ctc gcc	104
Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu Ala	
10 15 20	
cgg ctg cag gtg gct ttg cag atc gct cct cca tgt acc agt gag aag	152
Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys	
25 30 35	
cat tat gag cat ctg gga cgg tgc tgt aac aaa tgt gaa cca gga aag	200
His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys	
40 45 50	
tac atg tct tct aaa tgc act act acc tct gac agt gta tgt ctg ccc	248
Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro	
55 60 65 70	
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Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys	
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Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr	
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Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val	
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Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr	
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Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val	
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Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu	
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Pro Ala Arg Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu	
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Ile Ile Leu Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile	
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Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu	
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Trp His Trp Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu	
250 255 260	
tcc tca ggt gac agt tgt gtc agt aca cac acg gca aac ttt ggt cag	872
Ser Ser Gly Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln	
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Gln Gly Ala Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr	
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Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly	
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Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met	
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Met Pro Thr Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp	
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Ser Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe	
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Thr Gly Thr Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu	
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Pro Leu Cys Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu	
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Gln Lys Glu Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro	
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Ser Pro Asn Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly	
440 445 450	
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Glu Asp Cys Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro	

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Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg				
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Ser Ser Gly Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr				
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Gly Arg Pro Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala				
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Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu				
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Lys Ala				
615				
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<212> PRT
<213> Homo sapiens

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Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
35        40        45
Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
50        55        60
Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
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Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
85        90        95
Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
100       105       110
Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
115       120       125
Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
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Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
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Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
165       170       175
Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
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Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
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Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
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Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
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Ser	Cys	Asn	Cys	Thr	Glu	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met
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Ser	Ser	Glu	Asn	Tyr	Leu	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro
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His	Trp	Ala	Ala	Ser	Pro	Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly
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Cys	Arg	Asn	Pro	Pro	Gly	Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro
	450					455					460				
Lys	Arg	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro
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Glu	Glu	Glu	Ala	Ser	Arg	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly
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Ala	Asp	Gly	Arg	Leu	Pro	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly
			500					505					510		
Ser	Ser	Pro	Gly	Gly	Gln	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn
		515					520					525			
Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly
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Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala
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Ala	Ala	Ala	Glu	Pro	Met	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala
				565					570					575	
Arg	Arg	Asp	Ser	Phe	Ala	Gly	Asn	Gly	Pro	Arg	Phe	Pro	Asp	Pro	Cys
			580					585				590			
Gly	Gly	Pro	Glu	Gly	Leu	Arg	Glu	Pro	Glu	Lys	Ala	Ser	Arg	Pro	Val
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ctccccgcgc	actagaacga	gcaagtgata	atcaagttac	t atg agt ctg cta aac			236
				Met Ser Leu Leu Asn			
				1	5		

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Cys Glu Asn Ser Cys Gly Ser Ser Gln Ser Glu Ser Asp Cys Cys Val
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Ala Met Ala Ser Ser Cys Ser Ala Val Thr Lys Asp Asp Ser Val Gly

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cat tat gat cta gac tgc cct aca gcc cca att cca tgc aca ttc agt His Tyr Asp Leu Asp Cys Pro Thr Ala Pro Ile Pro Cys Thr Phe Ser 230 235 240 245			956
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Cys Met Arg Leu His Leu Gln Leu Pro Thr Ala Gln Arg Cys Ala Asn	
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Tyr Ile Ser Leu Phe Val His Thr Met Gln Gly Glu Tyr Asp Ser His	
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Pro Glu Leu Leu Ala Phe Gln Arg Pro Thr Ile Pro Arg Asn Pro Lys	
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 Val Gln Thr Pro Cys Gly His Arg Phe Cys Lys Ala Cys Ile Ile Lys
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 Pro Cys Thr Phe Ser Thr Phe Gly Cys His Glu Lys Met Gln Arg Asn


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<211> 316

<212> PRT

<213> Mus musculus

<400> 16

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 20           25           30
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
 35           40           45
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50           55           60
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65           70           75           80
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85           90           95
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100          105          110
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115          120          125
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130          135          140
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145          150          155          160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165          170          175
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180          185          190
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195          200          205
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His

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210		215		220	
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr					
225		230		235	240
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys					
	245		250		255
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr					
	260		265		270
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile					
	275		280		285
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala					
	290		295		300
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp					
305		310		315	

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